

FIGURE 1

GGCATCTGCCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGG
CTCTGTTGAGAATC**ATG**CTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTC
CTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCC
AGACTGCAGTAAGTGTGTGTCATGGAGACTACAGCTTTTCGAGGCTACCAAGGCCCCCCTGGGC
CACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGT
CATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGG
GCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCAT
TCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT
GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGG
TGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACC
TTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGAT
ACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGG
CAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTG
AAACTAAG**TAA**ATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGAT
TTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATT
GGTTGCAATGTTGTTACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAA
GAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCAC
TCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT
CACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTTCAGG
AACCCTGAAGTTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATA
TGACAGGGCTGGGGCAAGAACAGGGGCAGTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCG
TGTTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTC
ACATACAATGCTATTTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGG
TTGTAATTTTGTGTATGTTCCCCCACATCGCCCCAACTTCGGATGTGGGGTCAGGAGGTTG
AGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAA
ATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTT
AGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATAT
ATGGAAATAAACACACCTTTGTTAAAGATAAAAAAAA

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44686

><subunit 1 of 1, 246 aa, 1 stop

><MW: 26994, pI: 6.43, NX(S/T): 0

MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPP
GIPGNHGNNGNNGATGHEGAKGEKGDKGD LGPRGERGQHGPKEKGYPGIPPELQIAFMASL
ATHFSNQNSGII FSSVETNIGNFFDVMTGRFGAPVSGVYFFTF SMMKHEDVEEVYVYLMHNG
NTVFSMYSYEMKGKSDTSSNHA VLKLAKGDEVWLRMGNGALHGDHQR FSTFAGFLLFETK

Important features of the protein:

Signal peptide:

amino acids 1-22

Motif name: Clq domain signature.

amino acids 137-167

Clq domain proteins.

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75

FIGURE 3

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGG
CTCTGGCAGGCTCCTGGCAGCATGGCAGTGAAGCTTGGGACCCCTCCTGCTGGCCCTTGCCCT
GGGCCTGGCCCAGCCAGCCTCTGCCCCGCCGGAAGCTGCTGGTGTCTCTGCTGGATGGTTTTTC
GCTCAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTCAAAGAGATTGTGAGC
AGGGGAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTA
TACCCTAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACCTACATGTGGGACC
CCACCACCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGG
AATGGATCAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTA
CTGGCCAGGCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAA
ATGTCCCAACGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGT
GGCCGGGCGGACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGG
GCCTGCATCTCCGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGA
CCAAGTGGATCCAGGAGCGGGGCTGCAGGACCGCCTGAACGTCATTATTTCTCGGATCAC
GGAATGACCGACATTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAA
TGACCTGCAGCAAGTGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCTGGGAAAC
ACTCTGAGATATATAACAAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCC
ATCCCAAGCAGGTTCTATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGA
TGAAGGCTGGTTCATAACTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCA
GGCGGGAAGGTTGGCAGCGTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGC
ATCTTCCTGGCCTTCGGACCTGATTTCAAATCCAACCTCAGAGCTGCTCCTATCAGGTCGGT
GGACGTCTACAATGTCATGTGCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCT
GGTCCAGGGTGATGTGCATGCTGAAGGGCCGCGCCGGCACTGCCCCGCCTGTCTGGCCCAGC
CACTGTGCCCTGGCACTGATTCTTCTCTTCTGCTTGCATAACTGATCATATTGCTTGTCTC
AGAAAAAACACCATCAGCAAAGTGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGA
ATAATAGCTTCATTAACACAATCAAGACCATGCACATTGTAAATACATTATTCTTGGATAAT
TCTATACATAAAAGTTCCTACTTGTTAA

FIGURE 4

MAVKLGTLALLALGLAQPASARRKLLVFLLDGFRSDYISDEALESPLPGFKEIVSRGVKVDY
LTPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVNKDSLMLWWNGSEPLW
VTLTKAKRKVYMYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA
IYHERIDVEGHHYGPASPQRKDALKAVDVTVLKYMTKWIQERGLQDRNLNVIIFSDHGMTDIFW
MDKVIELNKYISLNDLQQVKDRGPVVSLLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYY
KKGKFVSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGP
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALI
LLFLLA

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

FIGURE 5

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCC
CCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGG
GGGCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCA
GGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGG
TGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAG
TGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACC
CTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGT
GCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG
CGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGCCCTGCTCCCGCGACGGCTCGGGGCT
CCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGGGCTGCACCT
GCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGC
TCCCCAGAGGGCACCCCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCAACACT
ACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTC
CAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAA
AAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTA
TCACTGGCCTCAGGCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCT
TAAACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACACATCCCCAAAA

FIGURE 6

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL
PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDYPQKL
AFAECLCRGCIDARTGRETAALNSVRLQLSLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVP
VGCTCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

FIGURE 7

CGGCCAGGGCGCCGACAGCCCGACCTCACCAGGAGAAC**ATG**CAGCTCGGCACTGGGCTCCTG
CTGGCCGCCGTCTTGAGCCTGCAGCTGGCTGCAGCCGAAGCCATATGGTGTCAACAGTGCAC
GGGCTTCGGAGGGTGCTCCCATGGATCCAGATGCCTGAGGGACTCCACCCACTGTGTACCA
CTGCCACCCGGGTCCTCAGCAACACCGAGGATTTGCCTCTGGTCACCAAGATGTGCCACATA
GGCTGCCCCGATATCCCCAGCCTGGGCCTGGGCCCCCTACGTATCCATCGCTTGCTGCCAGAC
CAGCCTCTGCAACCATGAC**TGA**CGGCTGCCCTCCTCCAGGCCCCCGGACGCTCAGCCCCAC
AGCCCCACAGCCTGGCGCCAGGGCTCACGGCCGCCCTCCCTCGAGACTGGCCAGCCCACC
TCTCCCGGCCTCTGCAGCCACCGTCCAGCACCGCTTGTCTAGGGAAGTCCTGCGTGGAGTC
TTGCCTCAATCTGCTGCCGTCCAAGCCTGGGGCCCATCGTGCCTGCCGCCCCCTCAGGTCCC
GACCTCCCCACAATAAAATGTGATTGGATCGTGTGGTACAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1000 900 800 700 600 500 400 300 200 100 0

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623

><subunit 1 of 1, 97 aa, 1 stop

><MW: 10160, pI: 6.56, NX(S/T): 0

MQLGTGLLLA AVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLP
LVTKMCHIGCPDIPSLGLGPYVSIACCQTSLCNHD

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

FIGURE 9

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCTCAGAGGCCGGGGAAGAGAAGCAAAG
CGCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCT
AACTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCG
CGGCACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTCTGGGCAG
CTGGGCTCGGGCGGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTC
GCGGGCTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG
CCGCG**ATG**AGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCC
TTCTGCCGCCGCGTGGTCAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTA
CAAAATGGCCTACTTCCATGAACTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTT
GTGAGAGTGAGGGAGGAGTCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAG
AGCATGTTGCAAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGG
GCTTTGGAGGAATGGAGATGGGCAACATCTGGTGCCTGCCAGATCTCTACCAGTGGTCTG
ATGGAAGCAATTCCAGTACCGAACTGGTACACAGATGAACCTTCCTGCGGAAGTGAAAAG
TGTGTTGTGATGTATCACCAACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCA
GTGGAATGATGACAGGTGTAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTA
ATCCAACAGCCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAAT
GTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACC
CCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCTGCATAAAAGTA
AAGGAAGAACAAAAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAA
GAAAGTGGCATGGAAGTA**TA**ATAACTCATTGACTTGGTTCCAGAATTTTGTAATTCTGGATC
TGTATAAGGAATGGCATCAGAACAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGCAA
GATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTATATGTCTATTATTTT
ATTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCAC
CCAACTTCAAACCTTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTC
GGGAGTATGTGTGTTAGAAGCAATTCCTTTTATTTCTTTTACCTTTCATAAGTTGTTATCTA
GTCAATGTAATGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAA
GTGTTTGATAAAAATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTTCAATACAT
GCTCTTTTGATTAAAGAACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAG
TACCATAGAAAAAGTTTGTCTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCA
ATGTCTAGGAAATCTCTTCAGAAATAAGAAGCTATTTCAATTAAGTGTGATATAAACCTCCTC
AAACATTTTACTTAGAGGCAAGGATTGTCTAATTTCAATTTGTGCAAGACATGTGCCTTATAA
TTATTTTGTAGCTTAAAATTAAACAGATTTTGTAAATAATGTAACCTTTGTTAATAGGTGCATAA
ACACTAATGCAGTCAATTTGAACAAAAGAAGTGACATACACAATATAAATCATATGTCTTCA
CACGTTGCCTATATAATGAGAAGCAGCTCTCTGAGGGTTCTGAAATCAATGTGGTCCCTCTC
TTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTTGGGATTGACACTGGAGGCAGATAGTTGC
AAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTGACTATATTAGTATACAAAGAGG
TCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAGACAAGCACAGCACACAGAC
ATTTTAGGAAGGAAGGAACACTACGAAATCGTGTGAAAATGGGTGGAAACCCATCAGTGATCG
CATATTCATTGATGAGGGTTTGTCTTGAGATAGAAAATGGTGGCTCCTTTCTGTCTTATCTCC
TAGTTTCTTCAATGCTTACGCCTTGTCTTCTCAAGAGAAAGTTGTAAGTCTCTGGTCTTCA
TATGTCCCTGTGCTCCTTTTAAACCAAATAAAGAGTTCTTGTCTTCTGGGGGAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79230

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30431, pI: 6.79, NX(S/T): 3

MSRVVSLLLGAALLCGHGAFRCRRVVSQGKVCFAFKHPCYKMAYFHELSSRVSFQEARLACE
SEGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSGACPDLYQWSDG
SNSQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINP
TAPVEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKG
RTKTSPNQSTLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145
and 212-217

FIGURE 11

GGAGAATCGAGAGAGCAGTGAAGTGGAGTCCGGGGTCTGGTCCGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG
CCACAGCCACTGGGCCCCAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTCTGTGCGAGGCCGGCAGGTGG
GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCTGACC
GGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCTAC
AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCAACGGAAAACAGCAGATCTTCTCCGTTTCAGAGGACT
GCCTGGTCCTCAACGTCTATAGCCAGCTGAGGTCCCCGCAGGGTCCGGTAGGCCGGTCATGGTATGGGTCCATG
GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGG
TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTACGACTGGAGATGAGCATGCACCTGGCAACCAGGGCT
TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA
CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTCC
ACAGAGCCATCACACAGAGTGGGGTTCATCACCACCCAGGGATCATCGACTCTCACCCTTGGCCCCCTAGCTCAGA
AAATCGCAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG
AAGAGCTGGTCTTAGCAAGAAGCTGAAAATACTATCTATCCTCTCACCCTTGATGGCACTGTCTTCCCCAAAA
GCCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCCCTCATGGGTGTCAACAACCATGAGTTCA
GCTGGCTCATCCCCAGGGGTGGGGTCTCCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT
CAACACCCGTCTTGACCAGTCTGGATGTGCCCCCTGAGATGATGCCACCGTCATAGATGAATACCTAGGAAGCA
ACTCGGACGCACAAGCCAAATGCCAGGCGTTCCAGGAATTCATGGGTGACGTATTCATCAATGTTCCCAACCGTCA
GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTTCTATGAGTTCAGCATCGACCCAGTTCTTTTG
CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGTCTTTGTGTTCGGAGGTCCCTTCCCTCA
TGGACGAGAGCTCCCGCCTGGCCTTTCAGAGGCCACAGAGGAGGAGAAGCAGCTAAGCCTCACCATGATGGCCC
AGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCCAATTCAACCAGGCGG
AACAAATATCTGGAGATCAACCCAGTGCCACGGGCGGACAGAAAGTTCAGGGAGGCCTGGATGCAGTTCTGGTCAG
AGACGCTCCCAGCAAGATAACAAGTGGCACCAGAAGCAGAAGAACAGGAAGGCCAGGAGGACCTCTGAGGCC
AGGCCTGAACCTTCTTGGCTGGGGCAAACCACTCTCAAGTGGTGGCAGAGTCCAGCACGGCAGCCCGCCTCTC
CCCCTGCTGAGACTTTAATCTCCACAGCCCTTAAAGTGTCCGGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA
ATGTCAAAAGGCCGCTCCACCTCTGGGGCATTTGTACAAGTTCTTCCCTCTCCCTGAAGTGCCTTTCTGCTTT
CTTCGTGGTAGGTTCTAGCACATTCCTCTAGCTTCTTGGAGGACTCACTCCCAGGAAGCCTTCCCTGCCTTCTC
TGGGCTGTGCGGGCCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT
CCCCCTCAGAGGAGCTCTCTCAAAATGGGGATTAGCCTAACCCCACTCTGTCACCACACACAGGATCGGGTGGGA
CCTGGAGCTAGGGGGTGTCTGTGAGTGAGTGAGTGAAACACAGAATATGGGAATGGCAGCTGCTGAACTTGAAC
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCCGACATTGTCCACCCTGGCCAGAAGGGTGCATGCC
AATGGCAGAGACCTGGGATGGGAGAAGTCTTGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCGTAC
TAAGGCCTCAGACTAGGGGCGGAGGGGTCTCCTCCTCTCTGCTGCCAGTCTGGCCCCCTGCACAAGACAACAGA
ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCCCTACCAATTCAGCCCCCTGACCCCTCAGGACGCTGGATG
CCAGCTCCCAGCCCCAGTGGCGGTCTCCTCCTCCTTCTTGGCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAG
AGCACCACCAAGACACAGCAGGACAGGGCAGGGGAGGGCATCTGGACCAGGGCATCCGTGGGGCTATTGTCA
GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACCAGAGGTTTTTCAGATGGAAGTGAGAG
GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGTCTCTCCCTGCCGCTCTGCTGGGCTCCCACTTTGGCA
GCACTTGAGGAGCCCTTCAACCCGCCGCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAGGCCGAGCCAGCT
CCCTCAGCTTGGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGGGGCCAG
AGTGAGTTCCGGGTGGGCGTGGGCTCGGCGGGGCCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCCT
TAGCACCTGGGGCAGCAGCTGCTGTGCTCGATTCTCGCTGGGCTTAGCTGCCTCCCCCGAGGGGCTCGG
GACCTGCAGCCCTCCATGCCTGACCCCTCCCCCACCCTCGTGGGCTCCTGTGCGGCCGAGCCTCCCCAAGGAG
CGCCGCCCTGCTCCACAGCGCCAGTCCCATCGACCACCCAAGGGCTGAGGAGTGGGGTGCACAGCGCGGGA
CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG
GGAATGGAGAACCTTTATGTCTAGCTAAGGGATTGTAAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTT
TGTAACACACCAATCAGCACCTGTGTCTAGCTCAGTGTGTGTGAATGCACCAATCCACACTCTGTATCTGGCT
ACTCTGGTGGGGACTTGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGATGTGGAGAACCT
TTGTGTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCTGTCAAACAGACCCTTGAATCTCTGTAAAT
GGACCAATCAGCAGGATGTGGTGGGGCAGACAAGAGAATAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC
CCCTCGGGTCCCCCACCAGCCGTGGAAGCTTTGTCTTTCGCTCTTGCATATAATCTTGCTACTGCCAAAA

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79862

><subunit 1 of 1, 571 aa, 1 stop

><MW: 62282, pI: 5.56, NX(S/T): 1

MERAVRVESGVLGVVCLLLACPATATGPEVAQPEVDTTLGRVGRQVGVKGTDRLVNVFLG
IPFAQPPLGPDREFSAPHPAQWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDC
LVLNVYSPAIEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAAYGDVVVVTVQYRLGVLGFF
STGDEHAPGNQGFLLDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIIISGLVLSPPVAAGLF
HRAITQSGVITTPGIIDSHPWPLAQKIAN TLACSSSSPAEMVQCLQQKEGEELVLSKKLKNT
IYPLTVDGTVPKSPKELLKEKPFHSVPFLMGVNNHEFSWLI PRGWGLLD TMEQMSREDMLA
ISTPVLTSLDVPPPEMMPTVIDEYLG SNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGS
PVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTM
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQW
HQKQKNRKAQEDL

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,
461-467

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

FIGURE 13

CATGGAGCCTCTTGCAGCTTACCCGCTAAATGTTCCGGGCCAGAGCAAAGGTATTTGCAG
TTTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAATTCCTCAA
CCTAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTTCTCT
GGAAAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAG
ACAGAAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCACCTCAGCGTG
TTGGCTTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCCAAGCAAGGAAGTAGAATC
TTTTGCAAGAAAAAACTACGGAGTAACTTTCCCCATCTTCCACAAGATTAAGATTCTAGGAT
CTGAAGGAGAACCTGCATTTAGATTTCTTGTGATTCTTCAAAGAAGGAACCAAGGTGGAAT
TTTTGGAAGTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCC
CATGAAGTCATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAG
AGGATCTAT**TGA**GAAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTG
GTCTCATTTTTAAACATTTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTG
CAGTAGTGCGTTCTCAGCTCATTGCAACCTCTGCCTTTTTTAAACATGCTATTAAATGTGGCA
ATGAAGGATTTTTTTTTTAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCCAGGATGAG
GATGTTACCCAAAGCAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAACACT
TCCTCTGACCATACTAAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTG
TTCAACTTGACATTTTCTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTT
GGATTCAAGAGCACTGTGTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATG
GAATAAAACACAAATGTTGAAAAATGTAAAATATATATACATAGATTCAAATCCTTATATAT
GTATGCTTGTTTTGTGTACAGGATTTTGTTTTTTCTTTTTTAAGTACAGGTTCTAGTGTTTT
ACTATAACTGTCACATATGTATGTAAGTACATATATAAATAGTCATTTATAAATGACCGTAT
TATAACATTTGAAAAAGTCTTCATCAAAAAAAAAAAAAA

[illegible]

MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTFLFLLQLKFLKPKINSFYAFEVKDAKGRVTSI
EKYKGKVSILVNVASDCQLTDRNYLGLKELHKEFGPSHFVLAFFPCNQFGESEPRPSKEVES
FARKNYGVTFPI FHKIKILGSEGEPAFRFLVDSKKEPRWNFWKYLVNPEGQVVKFWRPEEP
IEVIRPDIAALVRQVI IKKKEDL

amino acids 57-82

FIGURE 15

TGTGCGCTGGCCCTCGCCATGAGACCCCGCGAGCGTCCCCTCCCCGCGCCCTCCTGCTTCTGCTGCTGCTA
 CTGGGGGGCGCCACGGCCTCTTTCTGAGGAGCCGCGCGCTTAGCGTGGCCCCCAGGGACTACCTGAACCAC
 TATCCCGTGTGTTGTGGGCAGCGGGCCCGGACGCCTGACCCCGCAGAAGGTGCTGACGACCTCAACATCCAGCGA
 GTCTCTGCGGGTCAACAGGACGCTGTTTATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCAGC
 TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTGTGTGCGGATGAAG
 GGCAAACAGGAGGGCGAGTGTGAAACTTCGTAAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC
 GGTTCACACGCCTTCAACCCGGTGTGCGCCAACCTACAGCATAGACACCCTGCAGCCCGTCGGAGACAACATCAGC
 GGTATGGCCCGCTGCCCCGTACGACCCCAAGCAGCCTAATGTTGCCCTCTTCTCTGACGGGATGCTCTTACAGCT
 ACTGTTACCGACTTCTAGCCATTGATGCTGTATCTACCGCAGCCTCGGGGACAGGCCCACCCTGCGCACCCTG
 AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTC
 TTCCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCCGCGTGGCCCCGAGTGTGCAAGAAC
 GACGTGGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGTCCTTCTGAAGGCGCGGCTCAACTGCTGTGTA
 CCGGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGCGTGGTCAGCCTCGGGGGCGGGCCCGTG
 GTCCTGGCCGTTTTTTTCCACGCCCAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG
 GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCGAGTCCATCTGGACGCCGGTGGCGAGGATCAG
 GTGCCTCGACCCCGGGCCGGTGTGCGCAGCCCCCGGATGCAGTACAATGCCTCCAGCGCCTTGCCGGATGAC
 ATCCTCAACTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG
 CGGACCCTGATGAGGCACAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGGCCCCCTGGGGCAACCAGACCGTT
 GTCTTCTGGGTTCTGAGGCGGGGACGGTCTCAAGTTCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT
 GGGCTCAGTGTCTTCTGGAGGAGTTTGAAGCTTACCGGCCGGACAGGTGTGGACGGCCGGCGGTGGCGAGACA
 GGGCAGCGGCTGCTGAGCTTGGAGCTGGACGCAGCTTCGGGGGGCCTGCTGGCTGCCTTCCCCCGCTGCGTGGT
 CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTACAGACCCCTACTGC
 GGGTGGGCCCCCGACGGCTCCTGCATCTTCTCAGCCCGGGCACCAGAGCCGCTTTGAGCAGGACGTGTCGGG
 GCCAGCACCTCAGGCTTAGGGGACTGCACAGGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGTG
 TCGGTGAACCTGCTGGTAACGTGCTCGGTGGCGGCCTTCTGGTGGGAGCCGTGGTGTCCGGCTTACGCGTGGGC
 TGGTTCTGGGCGCTCCGTGAGCGGGCGGAGCTGGCCCGGCGCAAGGACAAGGAGGCCATCCTGGCGCACGGGGCG
 GGCGAGGCGGTGCTGAGCGTCAGCCGCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCGGGGGCGGAGGCGGT
 GGCGGTGGCGCCGGGGTTCCCCCGGAGGCCCTGCTGGCGCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG
 CTGCAGGGCGGGCCCCACGACCTGACTCGGGGCTGCTGCCACGCCCGAGCAGACGCCGCTGCCGAGAACGCGC
 CTGCCCCACTCCGCACCCGCACCCCCACGCCCTGGGCCCCCGCGCCTGGGACCACGGCCACCCCCCTGCTCCCCGCC
 TCCGCTTTCATCCTCCCTCCTGCTGCTGGCGCCCCCGGGCCCCCGAGCAGCCCCCGCGCCTGGGGAGCCGACC
 CCCGACGGCCGCTCTATGCTGCCCCGCGCGGCCGCGCCTCCACGGCGACTTCCCGCTCACCCCCACGCCAGC
 CCGGACCGCCGGCGGGTGGTGTCCGCGCCACGGGCCCCCTTGGACCCAGCCTCAGCCGCCGATGGCTTCCCGCGG
 CCGTGGAGCCCCGCCCCGACGGGCAGCCTGAGGAGGCCACTGGGCCCCACGCCCTCCGGCCGCCACCCTGCGC
 CGACCCACACGTTTCAACAGCGGCGAGGCCCGGCCCTGGGGACCGCCACCGCGGCTGCCACGCCCGGCCGGGACA
 GACTTGGCCACCTCCTCCCTATGGGGGGCGGACAGGACTGCGCCCCCGTGGCCTAGGCGGGGGCCCCCG
 ATGCCCTTGGCAGTGCCAGCCACGGGAACCAGGAGCGAGAGACGGTGCCAGAACGCCGGGGCCCCGGGGCAACTCCG
 AGTGGGTGCTCAAGTCCCCCCCCGCGACCCACCGCGGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACACCAG
 CTCGCCCTCCCCCTACCCGGGGCCGAGGACGCTGAGACGGTTTGGGGGTGGGTGGGCGGGAGGACTTTGCTATG
 GATTTGAGGTTGACCTTATGCGCGTAGGTTTTGTTTTTTTTTGCAGTTTTGGTTTTCTTTTGGGTTTTCTAAC
 AATTGCACAACTCCGTTCTCGGGGTGGCGGAGGAGGGGAGGCTTGGACGCCGGTGGGAATGGGGGGCCACAG
 CTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCCAACCCAGGCCCTGGCGTGTGTGGGTGTGCG
 TGCGTGTGCGTGCCGTGTTCTGTGTGCAAGGGGCGGGGAGGTGGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG
 TGGGCGTGTGTGTCAAGTGGGCGACGCTGAGGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC
 TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCCGGGGGTCTCCGAGGTGCCGGTTAGGAGTTTGAAC
 CCCCCCACTCTGCAGAGGGAAGCGGGGACAATGCCGGGGTTTCAGGCAGGAGACAGAGGAGGGCCTGCCCGGA
 AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCGTGGGGGGCGGCGAAGGTGGGTGGGGCCCCCTGTGTA
 ATACGGCCCCAGGGTGGTGAAGAGTCCCATGCCACCCGTCCCCTTGTGACCTCCCCCTATGACCTCCAGCTGA
 CCATGCATGCCACGTGGCTGGCTGGGTCTTGGCCTCTTGGAGTTTGCTCCCCAGCCCCCTCCCCATCAAT
 AAAACTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80145

><subunit 1 of 1, 888 aa, 1 stop

><MW: 95285, pI: 8.89, NX(S/T): 8

MQTPRASPPRPALLLLLLLLGGAHGLFPEEPPPLSVAPRDYLNHYPVFVVGSGPGRLTPAEGA
DDLNIQVRVLRVNRTLFIGDRDNLRYVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEG
ECRNFKVLLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALF
SDGMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSHVYFFFREI
AMEFNYLEKVVSRSVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTG
VVSLLGGRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTVPEDQVPR
PRPGCCAAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVAVDV
GAGPWGNQTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPDRCGRPGGGETGQ
RLLSLELDAASGGLLAAPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPG
TRAAFEQDVSGASTSGLGDCGTGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGW
FVGLRERRELARRKDKEAILAHGAGEAVLSVSRLGERRAQGPGRGGGGGGGAGVPPEALLA
PLMQNGWAKATLLQGGPHDLDGSLLPTEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLLP
SASSSLLLAPARAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDRRRVVSAPTG
PLDPASAADGLPRPWSPPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPG
TDLAHLPPYGGADRTAPPVP

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,
462-466

Glycosaminoglycan attachment sites.

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation sites.

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,
668-674, 669-675, 670-676, 868-874, 879-885

FIGURE 17

AGCAACTCAAGTTCATCATTGTCTGAGAGAGAGGAGCAGCGCGGTTCTCGGCCGGGACAGC
AGAACGCCAGGGGACCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCCTGGGGTCG
CGGAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTG
CGATCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTC
ATTTATCGGTGGATCATTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATT
GCTTCTTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCC
GAGAAGAGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTT
CTATATTCAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCT
TCCAGGTGAAAGTCTCAGCACCAGAGGAGCAATTCAGTAGAGTTGGAGTCCAGGTTTTAGAC
CGAAAAGATGGGTCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGT
GGAAATTAAATCCAAGGGCAACATGTGGCCAAATCCCATATATTTTAAAAGGGCCGGTTT
ACCATGAGAACTGTGACTGTCCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGC
CCTGAAACCATTGCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAA
GATTGCAGTAGAAATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAA
AGGATAACAAGGTTTATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTCATGGAT
GCCATACTACTTTCTTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTT
GGGAGACTGGCCTTTGGAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCCTGGT
GTGGCTCCACAGATTCCAAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTG
GAAACCATGGGCCGGGTAAAGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCTCCCTG
GGAAAGCAAAAATTCCTGCTGCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGC
TGGTTAACTCAGTAGAAAACACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTC
TTTAAACACGATGAAAACCTGTATGGTCCCATTGTGAAACATATTTTCAATTTTTTGATTTCTT
CAAGCATAAGTATCAAATAAATATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGC
TAGTTGGTGACAGTGTTGTGCTGAAGCAGGATTCCATCTACTATGAACATTTTTTACAATGAG
CTGCAGCCCTGGAAACACTACATTCCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAACT
TAAATGGGCGAAAGATCACGATGAAGAGGCCAAAAGATAGCAAAAGCAGGACAAGAATTTG
CAAGAAATAATCTCATGGGCGATGACATATTCTGTTATTATTTCAAACCTTTTCCAGGAATAT
GCCAATTTACAAGTGAGTGAGCCCCAAATCCGAGAGGGCATGAAAAGGGTAGAACCACAGAC
TGAGGACGACCTCTTCCCTTGTA CTTGCCATAGGAAAAAGACCAAAGATGAACTCTGATATG
CAAATAACTTCTATTAGAATAATGGTGCTCTGAAGACTCTTCTTAACTAAAAGAAGAATT
TTTTTAAGTATTAATTCCATGGACAATATAAAATCTGTGTGATTGTTTGCAGTATGAAGACA
CATTTCTACTTATGCAGTATTCTCATGACTGTACTTTAAAGTACATTTTTTAGAATTTTATAA
TAAAACCACCTTTATTTTAAAGGAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84917

><subunit 1 of 1, 502 aa, 1 stop

><MW: 58043, pI: 7.94, NX(S/T): 2

MFGTLLLYCFFLATVPALAEETGGERQLSPEKSEIWGPGLKADVVLPAFYFYIQAVDTSGNKF
TSSPGEKVFQVKVSAPEEQFTRVGQVLDKDGSEFIVRYRMYASYKNLKVEIKFQGQHVAKS
PYILKGPVYHENCDCPLQDSAAWLREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRFGQR
QSLCHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLDGWPLEKKKSNS
NIHPIFSWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGR
DSRKERLELVKLSRKHPOLIDAAFTNFFFFKHDENLYGPIVKHISFFDFFKHKYQINIDGTV
AAYRLPYLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKSNLSDLLEKLKWAKDHDEEAKK
IAKAGQEFARNNLMGDDIFCYFVKLFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRK
KTKDEL

Important features of the protein:

Signal peptide:

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

FIGURE 19

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCA
GCCTAGCGTGTCCACG**ATG**CGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCG
AGGTGCTAGGGATCGCGGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTTCGTTCTCTGCC
AGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGTTCTAACTG
GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG
ATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGGAA
AAAGGAGCATCTCACAGTTTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT
CAAGGCATTGATGACGGGGAGCCTTTCCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTC
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTT
TATGGAGATGAAACCTGGGTTAAATTATTCCTCAAAGCATTTCGTGGAATATGATGGAACAAC
CTCATTTTTTCGTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTTGGATAAAG
TATTA AAAAGAGGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGC
CACATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAGAAAGCTGAGCGAGATGGACAGCGTGCT
GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCTTTACCCAATTTGCTGG
TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG
GTGAATACACCTCTGATTTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA
TCCAAAGCACGTCCA**ATAG**ACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA
TTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAG
CAGTTGAGATTTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC
GTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTCAGAAAGATTGCATGGGAAC
GGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCCTATTCAACCTGGGCTCCAAGGTT
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCA
GTTCTCACCTGCTCCTGCTCAGCGTCCCACAGGCACCTGCACAGAAAGGCTGAGCTGGAAGT
CCCCTGTATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCG
TTCACGTCATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTG
GCGGCAGGCTGCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGG
CAGTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGG
TGTCCCGACACAGGTGTTACATCTGTGCTGTCAGGTGAGATGCCTCAGTTCTTGGAAGCT
AGGTTCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCC
CCCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGA
GGGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCAC
TCATCCTGCCACCCCCAGAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGA
CGTTTTCTGTTGGAATTCCTTAGTCCTTGGCCTCGGACACCTTCATTCGTTAGCTGGGGAGTG
GTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCAGGATCAAG
GGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCCTGCACAGCCCTCATC
CCCTCTTGGCTTGGCCGTGAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTT
TGTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACGCTTGACCTCGGGC
CCATCTGGGCTCATGCTCTCTCCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTA
GTTACCAAAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84920

><subunit 1 of 1, 310 aa, 1 stop

><MW: 33875, pI: 7.08, NX(S/T): 2

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSSARAEGAEPPAPEPSAGASSNWTTLPP
PLFSKVIVILIDALRDDFVFGSGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMT
GSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFEYDGTTSFFVS
DYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIGHISGPN SPLIGQKLSEMDSVLMKIHT
SLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 21

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATG**GCAAT
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATG
AAGCTGCCCAGCATCTCCTGTCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGA
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACCTGAC
AAATGCAACGCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
CACCACCGAGGGCACCACCAGCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT
CCCCGAGCACTACAGGTCCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGC
ATAGACCGCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGC
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLVVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIRTCHR
PSCCTTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 23

CCCACGCGTCCGGGACAGATGAACTTAAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGG
GAAAGGACAAAAAAGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCCTACTGCTGTTCT
TTTATGCTGGGAGCTGTGGCTGTAACCAACTAGGAAATAACGTATGCAGCAGCTATGGGCTGT
CAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCCTGTTTCTTTTTCTTTTTTGGGGAGTGT
CCTTGGCAGGTTCTGGGTTTGGACGTTATTTCGGTGACTGAGGAAACAGAGAAAGGATCCTTT
GTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCAG
GGTGGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCA
CAAATGAGAACTGGACCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTT
CAAATTTTAATGGATGATCCCTTTCAGATTTACCGGGCTGAGCTGAGAGTCAGGGATATAAA
TGATCACGCGCCAGTATTTTCAGGACAAAGAAACAGTCCTTAAAAATATCAGAAAATACAGCTG
AAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGGTATCCAA
AACTACACGATCAGCCCCAACTCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCAT
GATATATCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCT
TAACCCTCACAGCGCTGGATGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATC
GTTGTCTTGGACGTCAATGACAATGCCCCACAGTTTGCCAGGCTCTGTATGAGACCCAGGC
TCCAGAAAACAGCCCCATTGGGTTCCTTATTGTTAAGGTATGGGCAGAAGATGTAGACTCTG
GAGTCAACGCGGAAGTATCCTATTCAATTTTTTGATGCCTCAGAAAATATTCGAACGACCTTT
CAAATCAATCCTTTTTCTGGGGAAATCTTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAA
TTCTTACAAAATAAATATACAGGCAATGGACGGTGGAGGCCTTCTGCAAGATGTAGGGTTT
TAGTGGAAGTATTGGACACCAATGACAATCCCCCTGAACTGATCGTATCATCATTTTTCCAAC
TCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGCTGTTTTTAAGATTAATGACAGAGACTC
TGGAGAAAATGGAAAGATGGTTTGCTACATTCAAGAGAATCTGCCATTCTACTAAAACCTT
CTGTGGAGAATTTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGAG
TACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAAAT
AACGGTCTGGTCTCCGACGTCAATGACAACGCCCCCGCCTTACCCAAACCTCCTACACCC
TGTTTCGTCCGCGAGAACAACAGCCCCGCCCTGCACATCGGCAGCGTCAGCGCCACAGACAGA
GACTCGGGGACCAACGCCAGCTCACCTACTCGCTGCTGCCGCCCAAGACCCGCACCTGCC
CCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTCGCTGG
ACTACGAGGCCCTGCAGGCTTTCGAGTTCCGCGTGGGCGCCACAGACCGCGGCTCCCCGCG
CTGAGCAGAGAGGCGCTGGTGC GCGTGTGGTGCTGGACGCCAACGACAACCTCGCCCTTCGT
GCTGTACCCGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGC
CGGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTG
TCGTACCAGCTGCTCAAGGCCACGGAGCCCCGGGCTGTTTCGGTGTGTGGGCGCACAATGGGGA
GGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGCAGCCAAGCACAGGCTCGTGGTGCTTG
TCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGAC
GGCTTCTCCCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCGGCCAGGCCAGGCCGAGGC
CGACTTGCTCACCGTCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCCTCT
CGGTGCTCCTGTTTCGTGGCGGTGCGGCTGTGCAGGAGGAGCAGGGCGGCCTCGGTGGGTGCG
TGCTCGGTGCCCGAGGGTCTTTTTCCAGGGCATCTGGTGGACGTGAGGGGCGCTGAGACCCT
GTCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCGGGACCAGTGAGTTCAAGT
TCTTGAAACCAGTTATTTTCGGATATTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAAT
TCCACCTTCCGAAATAGCTTTGGATTTAATATTCAGTAAAGTCTGTTTTTGTAGTTTCATATAC
TTTTGGTGTGTTACATAGCCATGTTTCTATTAGTTTACTTTTTAAATCTCAAATTTAAGTTAT
TATGCAACTTCAAGCATTATTTTCAAGTAGTATACCCCTGTGGTTTTACAATGTTTCATCAT
TTTTTTGCATTAATAACAACCTGGGTTTAATTTAATGAGTATTTTTTTCTAAATGATAGTGT
AAGGTTTTAATTCCTTTCCAACGCCCCAAGGAATTAATTACTATTATATCTCATTACAGAAAT
CTGAGGTTTTGATTCATTTTCAGAGCTTGCACTCATGATTCTAATCACTTCTGTCTATAGTG
TACTTGCTCTATTTAAGAAGGCATATCTACATTTCCAAACTCATTCTAACATTCTATATATT
CGTGTGTTGAAAACCATGTCATTTATTTCTACATCATGTATTTAAAAAGAAATATTTCTCTAC
TACTATGCTCATGACAAAATGAAACAAAGCATATTTGTGAGCAATACTGAACATCAATAATAC
CCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTTGGCCAATATTTT
CTTATGTTAACTTTTTGCTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATA
ATCTGCCTGAAAATGAATAAAAATAAAACATTTTGAAATGTGAAAAA

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

MAVRELCFPRQRQVLFLFLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAAR
GTRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVR
DINDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGLNGIQNYTISPNSFFHINISGGD
EGMIYPELVLDKALDREEQGELSLLTALDGGSPSRSGTSTVRIVLVDVNDNAPQFAQALYE
TQAPENSPIGFLIVKVAEDVDSGVNAEVSYSFFDASENIRTTFQINPFSGEIFLRELLDYE
LVNSYKINIQAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKIND
RDSGENGMVCYIQENLPFLKPSVENFYILITEGALDREIRAEYNITITVTDLGTPLRKTE
HNITVLVSDVNDNAPAFQTQSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQDP
HLPLASLV SINADNGHLFALRSLDYEALQAFEFVVGATDRGSPALSREALVRVLVDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDGFSQPYLPLPEAAPAQ
AEADLLTVYLVVALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGHLVDVRGA
ETLSQSYQYEVCLTGGPGTSEFKFLKPVISDIQAQGPGRKGEE NSTFRNSFGFNIQ

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

Amidation site.

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92234

><subunit 1 of 1, 507 aa, 1 stop

><MW: 56692, pI: 5.22, NX(S/T): 3

MDPKLGRMAASLLAVLLLLLLERGMFSSSPPPPALLEKVQYIDLHQDEFVQTLKEWVAIESD
SVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQQLPDGQSLPIPPVILAELGSDPTK
GTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD
LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY
FMVEVKCRDQDFHSGTFFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY
KAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGK
FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAI
RTVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF
AAFFLEMAQLH

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

273-292

N-glycosylation sites.

amino acids 322-326, 382-386, 402-406

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 400-404

N-myristoylation sites.

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269,
351-357

Cell attachment sequence.

amino acids 140-143

ArgE / dapE / ACY1 / CPG:

amino acids 156-167

FIGURE 27

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCC
CGAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTC**ATG**GGACCTGTGCGGTT
GGGAATATTGCTTTTCTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGG
AGGACGATGACACAGAACGCTTGCCCAGCAAATGCGAAGTGTAAGCTGCTGAGCACAGAG
CTACAGGCGGAAGTGAAGTGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCT
GGATACAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGG
CCTTAGAGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCA
CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGAGAAGGG
GGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACAT
ACCTCAAGAAGCAGTGAGAGCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTAC
TTCCACCATCAGGAGCAGCCCCCTACAAAATTTTCTCTGTGAAGGTCATGTGCTCCCAGCTGC
TGAAACTGCATGTCTACAGGAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAA
CAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAG
ATGACCAAGACAGGAAGCCACCCCAAACCTTGACCGAGAAGATCTT**TGA**CCCTTGCCTTTGAG
CCCCCAGGAGGGGAAGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAG
CTTTCAGGGTGTGTTTATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACC
TCAGGCAAGATCCTGGTGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGG
TCCTGCTCCTAGAGATGAACTCTATÇCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTA
CTGAAAGCTTTCCTCTTTAACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGC
TGTGGGCTTTGGGGAAGTCACTTAGCTCCTTAAGGTCTGTTTTTTAGACCCTTCCAAGGAAGA
GGCCAGAACGGACATTCTCTGCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCA
GCAAACCGTGAAGGAGAATGGGACACTGGGTGATGGCCTGGAGTTGCTGATAATTTAGGTGG
GATAGATACTTGGTCTACTTAAGCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGT
GCTCAACTTTCTATATCGCTATTAACTTTTTTCTTTTTTTCTA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256

><subunit 1 of 1, 248 aa, 1 stop

><MW: 28310, pI: 4.63, NX(S/T): 0

MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVL
ELGQVLDTGKRKRHVPYSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMATLK
GLVQKGVKVDLGIPLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEG
HVLPAETAQLQETWTGKEITDGEEKTEGEEEEEEEEEEEEEGGDKMTKTGSHPKLDREDL

Important features of the protein:

Signal peptide:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

FIGURE 29

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT
CTCCCTGTGCTTAACCAGAGGTGCCC**ATG**GGTTGGACAATGAGGCTGGTCACAGCAGCACTG
TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGA
GGCCCTCTTGGACGAGGACACCCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGG
GGAACATTGGCTGCAAGGTTGTTCTGATTGTAACAACCTACAGACAGAAGATCACCTCCTGG
ATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGT
GGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA
CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAAGGGCCAGGAGTTATCAGCCTAC
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCA
GGAAGGAAAAGTCATCTCTCTCTCTTCCCAAGGAAAACAAAACCTCGAGGCTCTTGGAATGG
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAG
AACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA
AACCAGGCAGAGA**TAG**CTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC
TGCTCACCACCGACGATGTGGGTATGGAACCCCTCTGGATACAGAACCCCTTCTTTTCCAA
ATTAAAAAAAAAATCATCAA

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274

><subunit 1 of 1, 223 aa, 1 stop

><MW: 25402, pI: 8.14, NX(S/T): 1

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVP
DCNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLK
KGKIQQQELSAIQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRFLNRFHL
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 169-173

Tyrosine kinase phosphorylation site.

amino acids 59-68

N-myristoylation sites.

amino acids 54-60, 83-89, 130-136

Phosphatidylethanolamine signature.

amino acids 113-157

FIGURE 31

GTCGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTTCAGTCCCCTGGACTGTAGATAAAGA
CCCTTTCTTGCCAGGTGCTGAGACAACCACACTATGAGAGGCACTCCAGGAGACGCTGATGG
TGGAGGAAGGGCCGTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATCCAGAGG
CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTG
TATTGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCT
GTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT
CCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATTGCCTCCTCCAAGAGAGACCAGCCC
ATCATTCTGACTTCAGAACTTGGAAGTCATACAACACTGCCTTTGAATTAAATATAAATGA
CTGAACTCAGCCTAGAGGTGGCAGCTTGGTCTTTGTCTTAAAGTTTCTGGTTCCCAATGTGT
TTTCGTCTACATTTTCTTAGTGTCAATTTTCACGCTGGTGCTGAGACAGGAGCAAGGCTGCTG
TTATCATCTCATTTTATAATGAAGAAGAAGCAATTACTTCATAGCAACTGAAGAACAGGATG
TGGCCTCAGAAGCAGGAGAGCTGGGTGGTATAAGGCTGTCTCTCAAGCTGGTGCTGTGTAG
GCCACAAGGCATCTGCATGAGTGACTTTAAGACTCAAAGACCAAACACTGAGCTTTCTTCTA
GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACA
GAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCATCCAGTCTTTAT
ATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAAGACCTTGTAACA
AAAATAATTCTTGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGC
ATGACTAGCACAGAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCA
TCCAGTCTTTATATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAAG
ACCTTGTAACAATAAATAATTCTTGTGTTAAGTTAAATCATTTTTGTCTAATTGTAATGTG
TAATCTTAAAGTTAAATAAACTTTGTGTATTTATATAATAATAAAGCTAAAACCTGATATAAA
ATAAAGAAAGAGTAAACTG

FIGURE 32

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIONPEMCLYCEKVGEQPTL
QLKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY
NTAFELNIND

Signal sequence:

amino acids 1-17

N-myristoylation site.

amino acids 10-16

Cell attachment sequence.

amino acids 36-39

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIONPEMCLYCEKVGEQPTL
QLKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY
NTAFELNIND

FIGURE 33

GCGAGGCTGCACCAGCGCCTGGCACCATGAGGACGCCTGGGCCTCTGCCCCTGCTGCTGCTG
CTCCTGGCGGGAGCCCCGCGCGCGGCCCACTCCCCGACCTGCTACTCCCGCATGCGGGC
CCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGGAGCCCTCGGAGCCAT
GTGTGAGATACCTGCCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGGACAAGCTG
CGGGACTTTGTGGCCTCGCCCCCGTGTTGGAAAGTGGCCCAGGTAGATTCCCTTGAAGGACAA
AGCACGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTTGGTATTCCTGTTGG
ATGACTGCAATGCCTTGAATACCCAATCCCAGTGACTACGGTCCTGCCAGATCGTCAGCGC
TAAGGGAACTGAGACCAGAGAAAGAACCCAAGAGAACTAAAGTTATGTCAGCTACCCAGACT
TAATGGGCCAGAGCCATGACCCTCACAGGTCTTGTGTTAGTTGTATCTGAAACTGTTATGTA
TCTCTCTACCTTCTGGAAAACAGGGCTGGTATTCCTACCCAGGAACCTCCTTTGAGCATAGA
GTTAGCAACCATGCTTCTCATTCCTTGACTCATGTCTTGCCAGGATGGTTAGATACACAGC
ATGTTGATTTGGTCACTAAAAAGAAGAAAAGGACTAACAAGCTTCACTTTTATGAACAATA
TTTTGAGAACATGCACAATAGTATGTTTTTATTACTGGTTTAATGGAGTAATGGTACTTTTA
TTCTTTCTTGATAGAAACCTGCTTACATTTAACCAAGCTTCTATTATGCCTTTTTCTAACAC
AGACTTCTTCACTGTCTTTCATTTAAAAAGAAATTAATGCTCTTAAGATATATATTTTACG
TAGTGCTGACAGGACCCACTCTTTCATTGAAAGGTGATGAAAATCAAATAAAGAATCTCTTC
ACATGGA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA93011

><subunit 1 of 1, 136 aa, 1 stop

><MW: 15577, pI: 8.88, NX(S/T): 0

MRTPGPLPVLLLLLAGAPAAPPTPPTCYSRMRALSQEITRDFNLLQVSEPSEPCVRYLPRLY
LDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLLDDCNALEY P
IPVTTVLPDRQR

Important features of the protein:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site.

amino acids 60-69

N-myristoylation site.

amino acids 16-22

FIGURE 35

GTCTCCGCGTCACAGGAACTTCAGCACCCACAGGGCGGACAGCGCTCCCCCTCTACCTGGAGA
CTTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCA
GCCGCCAGTCCCGGCCCCCTCTCCCGCCCCACACCCACCCCTCCTGGCTCTTCCTGTTTTTAC
TCCTCCTTTTTCATTACATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCA
AGCCGAGCGTGGAAGA**ATG**GGGTTCCTCGGGACCGGCACTTGGATTCTGGTGTAGTGCTCC
CGATTCAAGCTTTCCCCAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTA
AGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAAC
ATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTTTGTGATAACTTGAACCTGC
TAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCA
CTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGA
TTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATC
AACTAGACGGGACTCCTTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTAT
GAAGAAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTAT
CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCT
CAAAGGAAGCCAACAATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAG
GCTGGAAAAATACCAGAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGG
AGAAAACGATGAAACAGTATCTAACACATTAACCTTGACAAATGGCTTGGAAGGAGAACTA
AAACCTACAGTGAAGACAACCTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTG
AAAAGTATTGATTGAGAAAAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAAC
ACTGATTGACTTTTGTGAAGATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTT
CCTACCTTGAAAACCTTGATGAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAAT
GCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGA
CAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAA
AAGATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTAT
TTGGAAGCCATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAAATAAAGA
AGATTATGACCTTTCAAAGATGAGAGACTTCATCAATAAACAGCTGATGCTTATGTGGAGA
AAGGCATCCTTGACAAGGAAGAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCT**GTAAAA**
TGGCAAAAGATCCAGGAGTCTTTCAACTGTTTCAGAAAACATAATATAGCTTAAACACTTC
TAATTCTGTGATTAAATTTTTTGACCCAAGGGTTATTAGAAAGTGCTGAATTTACAGTAGT
TAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT
TGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 36

MGFLGTGTWILVLVLPIQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPEN
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTK
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQA
HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPKVT PMAAIQDGLAKGENDET
VSNTLTLTNGLERRTKTYSEDNFEELQYFPN FYALLKSIDSEKEAKEKETLITIMKTLIDFV
KMMVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLS
KMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

[illegible][illegible]

FIGURE 38

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPR
LAWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVIL
NVQFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLDAQN
YPWLTNHTVQLQLRSLAHNLSVVATNDVGVTSASLPAPGPSRHPSLISSDSNNLKLNNVRLP
RENMSLP SNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIY
RVSSVSSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

FIGURE 39

CGGGGACGGAAGCGGCCCTGGGCCCAGAGGGGCTGGAGCCGGGCCGGGGCG**ATG**TGGAGCGC
GGGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGG
GCGGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTC
AATACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCA
GCAATCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCG
GCTCGGAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACG
CATGTGCTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCA
GGAGGTGAGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCT
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTG
TTCCTGTCAGTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGG
CATGCCCAGTGCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTA
GTGTGGAGCCCTCTGCAGGTCACGATGAACTC**TGAG**TGTGTGGATGGATGGGTGGATGGAGG
GTGGCAGGTGGGGCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTC
AAGTGCCTTTGTGATTAAAGAATGTTGGTCTATGAAA

FIGURE 40

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857

><subunit 1 of 1, 221 aa, 1 stop

><MW: 23598, pI: 6.96, NX(S/T): 0

MWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGS
GSGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSP
SNNQEVSAFGEDGEGDDLDLWTVRCGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQH
EVHGMP SANTHNTWKAMEGIFIKPSVEPSAGHDEL

Important features of the protein:

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196

Endoplasmic reticulum targeting sequence.

amino acids 218-223

FIGURE 41

GTTGCTATGTTGCCCAGGCTGGTCTTGAAGTGCCTTGACCTCCTAAAGTGTTGGAACCACAG
ACGTGAGCCACTCCACCCAGCCTAAAACTTCATCTTCTTTGGATGAGATGAACACTTTTAAC
AAGAGAACAGGACTCTATATAAATCGCTGTGGGCTCACCACCTCTAAGGAGGAGCACTGACT
GAAGACAGAAAAATTGATGAACTGAAGAAGACATGGTCCATTATGCCTTACAACTTACACA
GTGCTTTGGGAATTCCAAAGTACTCAGTGGAGAGAGGTGTTTCAGGAGCCGTAGAGCCAGAT
CGTCATC**ATG**TCTGCATTGTGGCTGCTGCTGGGCCTCCTTGCCCTGATGGACTTGTCTGAAA
GCAGCAACTGGGGATGCTATGGAAACATCCAAAGCCTGGACACCCCTGGAGCATCTTGTGGG
ATTGGAAGACGTCACGGCCTGAACTACTGTGGAGTTTCGTGCTTCTGAAAGGCTGGCTGAAAT
AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATTTGGCCAAAAGTACTGCA
TGGATCCTGCCGTGATCGCTGGTGTCTTGTCCAGGAAGTCTCCCGGTGACAAAATTCTGGTC
AACATGGGCGATAGGACTAGCATGGTGCAGGACCCTGGCTCTCAAGCTCCCACATCCTGGAT
TAGTGAGTCTCAGGTTTCCCAGACAACCTGAAGTTCTGACTACTAGAATCAAAGAAATCCAGA
GGAGGTTTCCAACCTGGACCCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCTACAGTGGG
GGTGCTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTTCTGCAATGATGTCCTTGC
ACGAGCCAAGTACCTCAAGAGACATGGCTTC**TAA**CATCTCAGATGAAACCCAAGACCATGAT
CACATATGCAGCCTCAAATGTTACACAGATAAACTAGCCAAGGGCACCTGTAACCTGGGAAT
CTGAGTTTGACCTAAAAGTCATTAAAATAACATGAATCCCATTAATAAAAAAAAAAAAAA

FIGURE 42

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867

.><subunit 1 of 1, 194 aa, 1 stop

><MW: 21431, pI: 8.57, NX(S/T): 0

MSALWLLLGLLALMDLSESSNWGCYGNIQSLDTPGASCGIGRRHGLNYCGVRASERLAEIDM
PYLLKYQPMMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDPGSQAPTSWISE
SQVSQTTEVLTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCNDVLARA
KYLKRHGF

Important features of the protein:

Signal peptide:

amino acids 1-19

N-myristoylation sites.

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

Amidation site.

amino acids 40-44

FIGURE 43

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCCTCGCC**ATG**AAAG
CCCTTATGCTGCTCACCCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCAC
TCCTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGG
ACAGCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCT
GTGGCACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTG
ACATATAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCC
AGCCCTGGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCAC**TGAG**
ACTCATTCCATTGGCTGCCCCCTCCTCCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCT
CTGTATCCCCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTG
TTCCGAGTGGTCTCCTCATCCATCCTTCCCACCTCACACCCTTCACTCTCCTTTTTCTGGGT
CCCTTCCCCTTCCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCT
ATACTCTGCTGTCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTG
TTGTCCCCAGTGAAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCA
AAGGCTCCCATATGTACCCCATCCCCATACTCACCTCTTCCATTTTGAGTAATAAA
TGTCTGAGTCTGGAAAAAAAAAAAAAAAAAAAA

FIGURE 44

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878

><subunit 1 of 1, 125 aa, 1 stop

><MW: 13821, pI: 8.60, NX(S/T): 2

MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSN
LRCGTPEEPCQEA FNQTNRKLG LTYNTTCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

Important features of the protein:

Signal peptide:

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

FIGURE 45

ACGGGCCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCA
GTCGGGCCGTTTCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCT
ACCGCACCCAGGTTTCGGCCCCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAGCGCCAT
CGCCGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCATTTGTTTC
TGCTGACCGCGGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTA
AAAGCTCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACA
GTTGAAATGTGTTGGAGGCACAGCTGGTGTGATTCTTATACCCCAAAGTCATACAGTGTC
AGAACAAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA
TACAAATTTGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGT
ACTAAGAGGTTCTTGTGGCTTGAGTATAATTTAGATTATACAGAAGTTGGCCTGCAGAAAC
TGAAGGAGTCTGGAAAGCAGCACGGCTTTGCCTCTTTCTCTGATTATTATTATAAGTGGTCC
TCGGCGGATTTCCTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTT
TGTAAGTCTATAAGCTGTTCCCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATC
CTCCATTTTCCCACCGTTACCAGAGATTACCAACTCAGCAGGACCTCCTCCCCCAGGCTTT
AAGTCTGAGTTCACAGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTTGGCAGTGC
TTTTACAGGACAACAAGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACTG
GTGGAATACTAGGATATTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGG
TACTACCCGTCCTATCCTCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCA
TGGAGGCTCGGGCAGCTATTTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAG
GATATGGTGGTACCAGGAGACGATAAAGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAAT
TTTGGATTTTTTCATCACTTTCTTTTAGAAAAAAGTACTACCTGTTAACAATTGGGAAAAG
GGGATATTCAAAGTTCTGTGGTGTATGTCCAGTGTAGCTTTTTTGATTCTATTATTTGAG
GCTAAAAGTTGATGTGTGACAAAATACTTATGTGTTGTATGTCAGTGTAAACATGCAGATGTA
TATTGCAGTTTTTGAAGTGATCATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAAAC
CTGTGATGCCCTAAGAAGCATTAAGAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAA
AATTTTCAGTTTTAGGTGGTTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTA
TTTGGTATTATATTATTTGATGTTTGCTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAA
TTATGCTAATTTGTGAGTTCTGATCACTTTTGAGCTCTGAAGCTTTGAATCATTCAGTGGTG
GAGATGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTA
GAAGGTGTTGTGAATGACTCTGTGCTGGCAAAAATGCTTGAAACCTCTATATTTCTTTTCGT
TCATAAGAGGTAAAGGTCAAATTTTTCAACAAAAGTCTTTTAATAACAAAAGCATGCAGTTC
TCTGTGAAATCTCAAATATTGTTGTAATAGTCTGTTTCAATCTTAAAAAGAATCA

FIGURE 46

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889

><subunit 1 of 1, 339 aa, 1 stop

><MW: 36975, pI: 7.85, NX(S/T): 1

MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIP
QLKCVGGTAGCDSYTPKVIQCQNKGDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQY
VLRGSCGLEYNLDYTELGQLKESGKQHGFAFSFYKSSADSCNMSGITIVVLLGIA
FVVYKLFSLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGS
AFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSPSYPGTWNRAYSPL
HGGSGSYSVCSNSDTKTRTASGYGGTRRR

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318